

1. *Phylogenetic relationships*—Phylogenetic relationships among the 12 species were determined using the parsimony method of Farris (1993) with the computer program PAUP (version 4.0a) (Nelson and Platnick, 1991). The parsimony method was chosen because of the lack of a priori knowledge of the evolutionary relationships among the species. The parsimony method was used to determine the most parsimonious tree (MPT) for the 12 species. The MPT was determined by using the following criteria: (1) the tree with the fewest steps; (2) the tree with the fewest homoplasies; (3) the tree with the fewest synapomorphies; and (4) the tree with the fewest apomorphies. The MPT was determined by using the following criteria: (1) the tree with the fewest steps; (2) the tree with the fewest homoplasies; (3) the tree with the fewest synapomorphies; and (4) the tree with the fewest apomorphies. The MPT was determined by using the following criteria: (1) the tree with the fewest steps; (2) the tree with the fewest homoplasies; (3) the tree with the fewest synapomorphies; and (4) the tree with the fewest apomorphies.

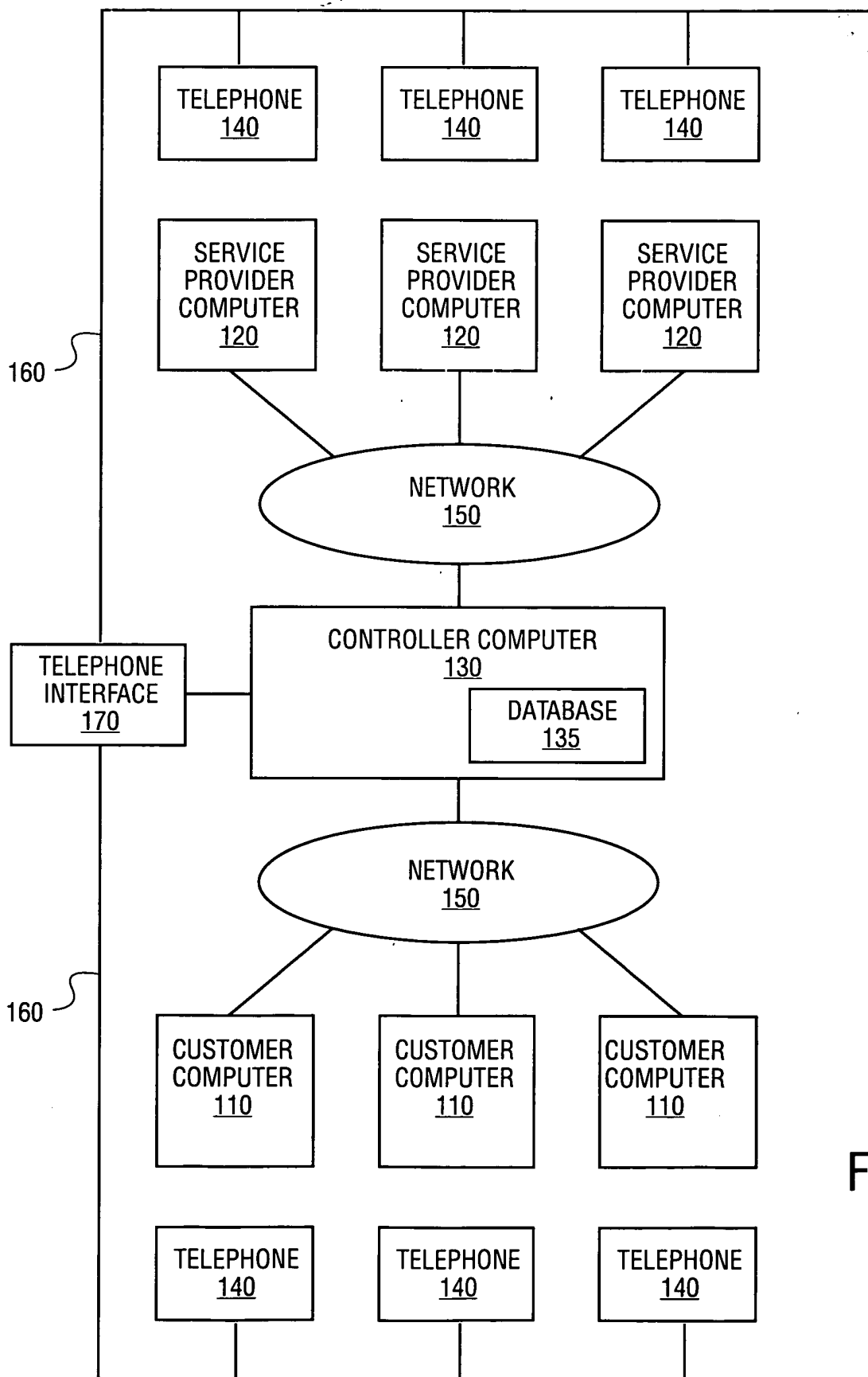


FIG. 2

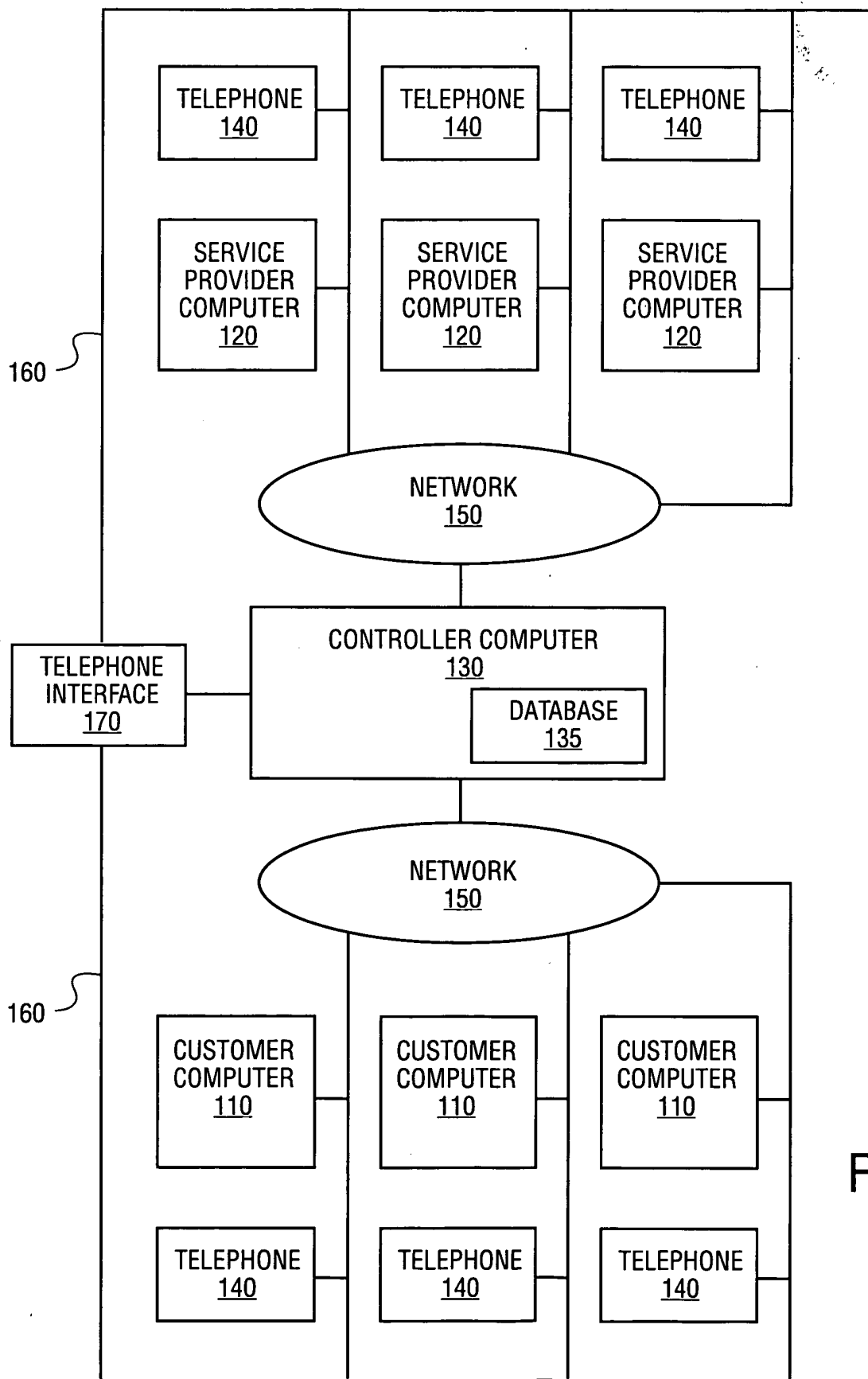


FIG. 2



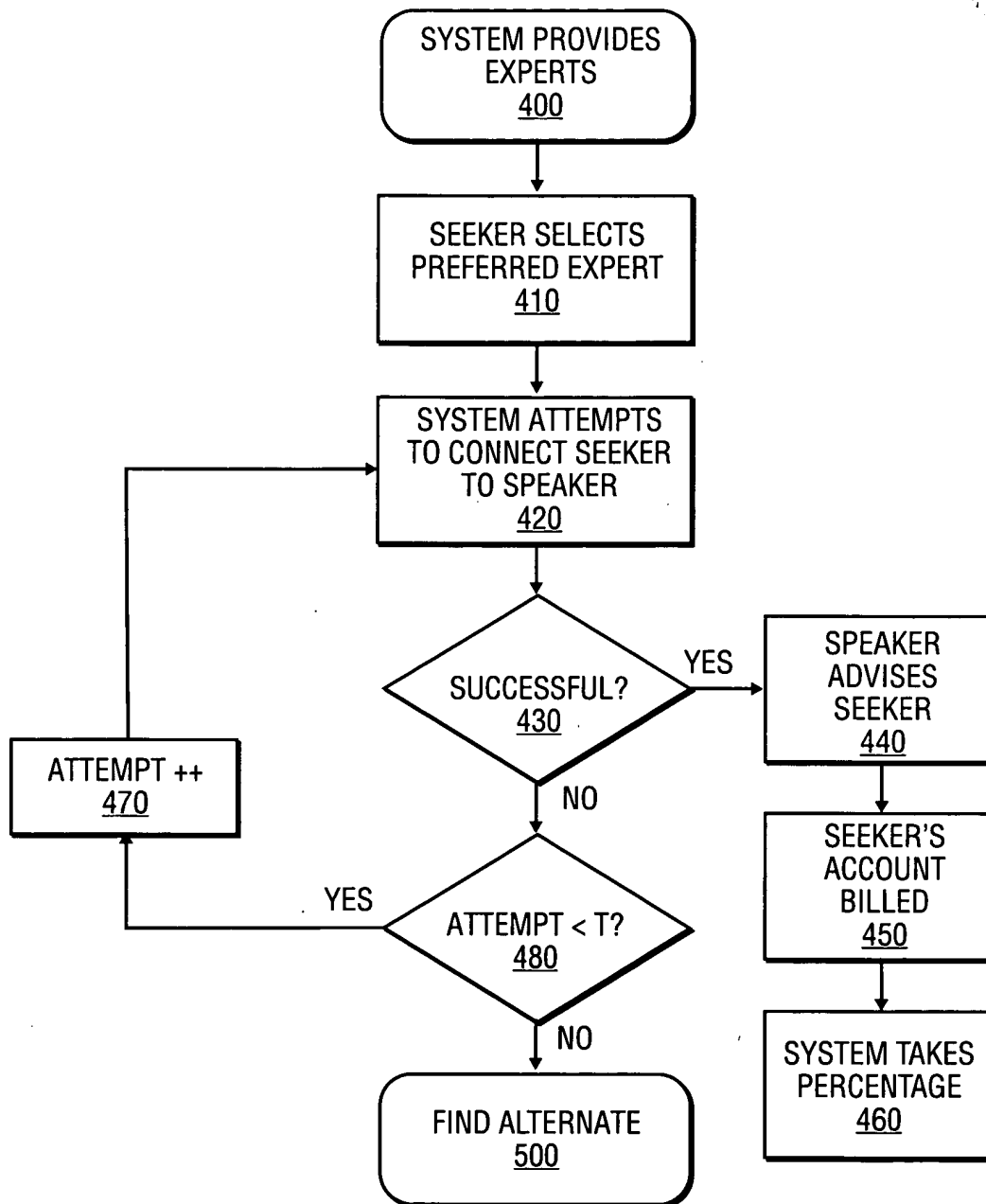


FIG. 4

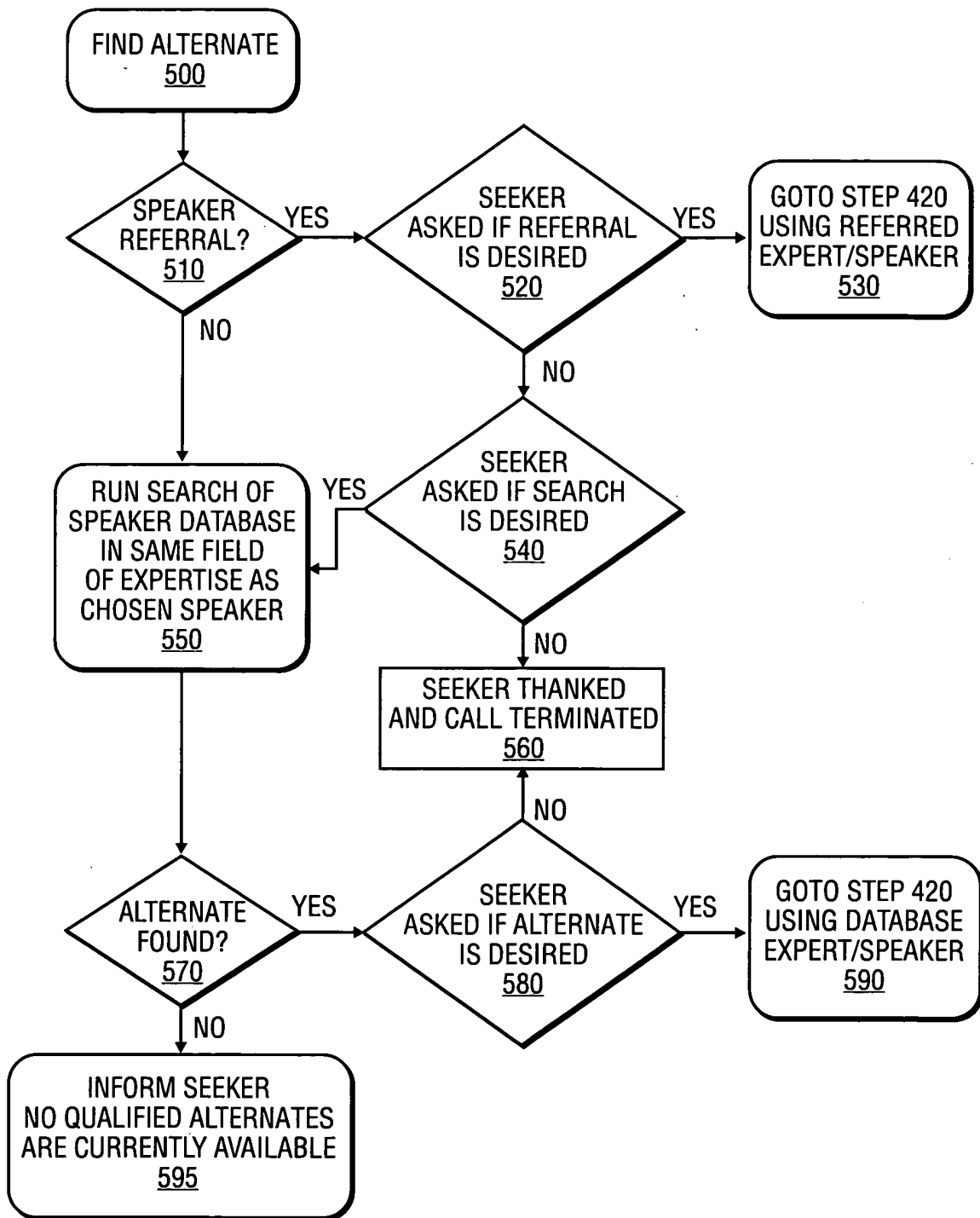


FIG. 5

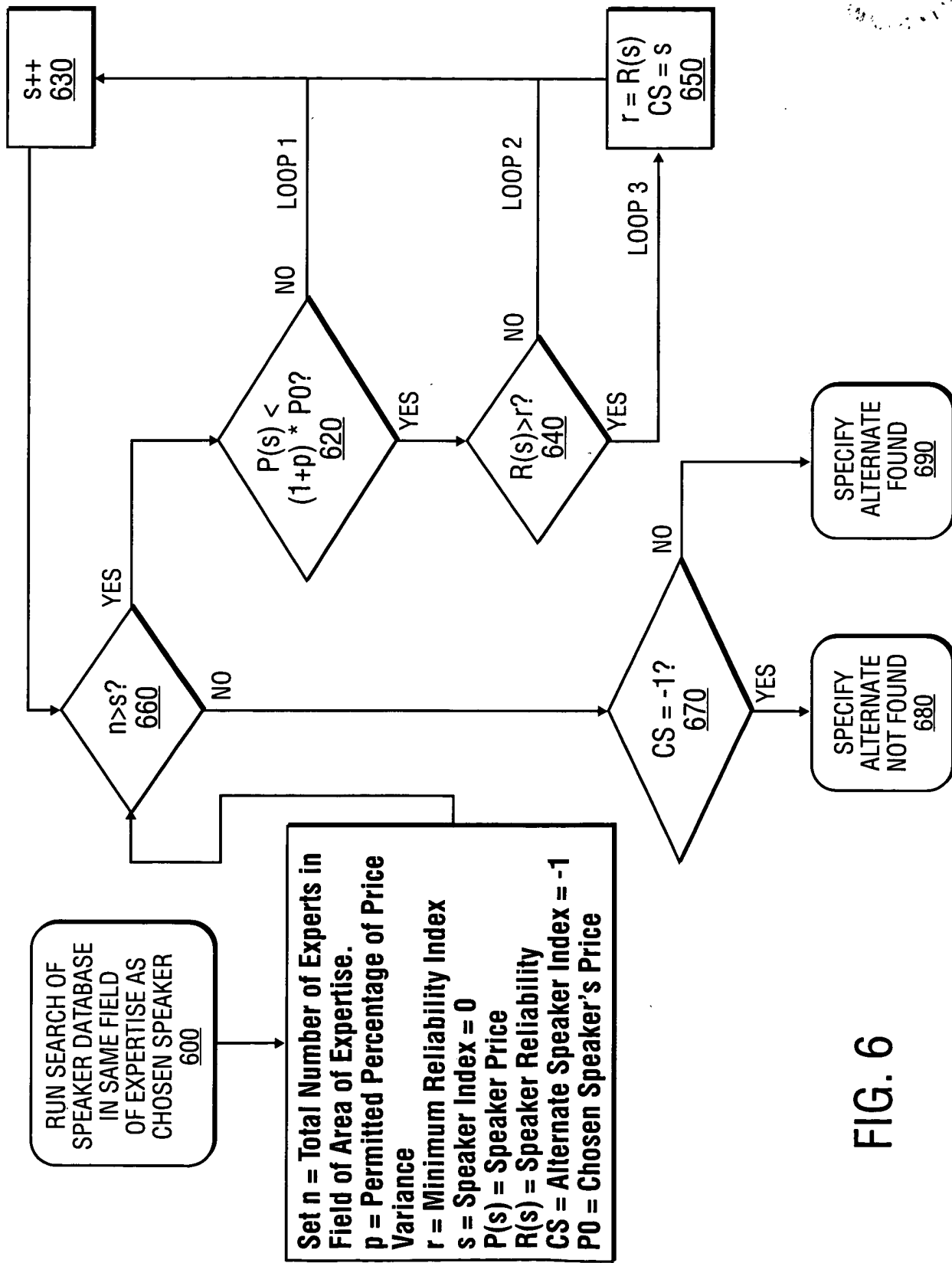


FIG. 6

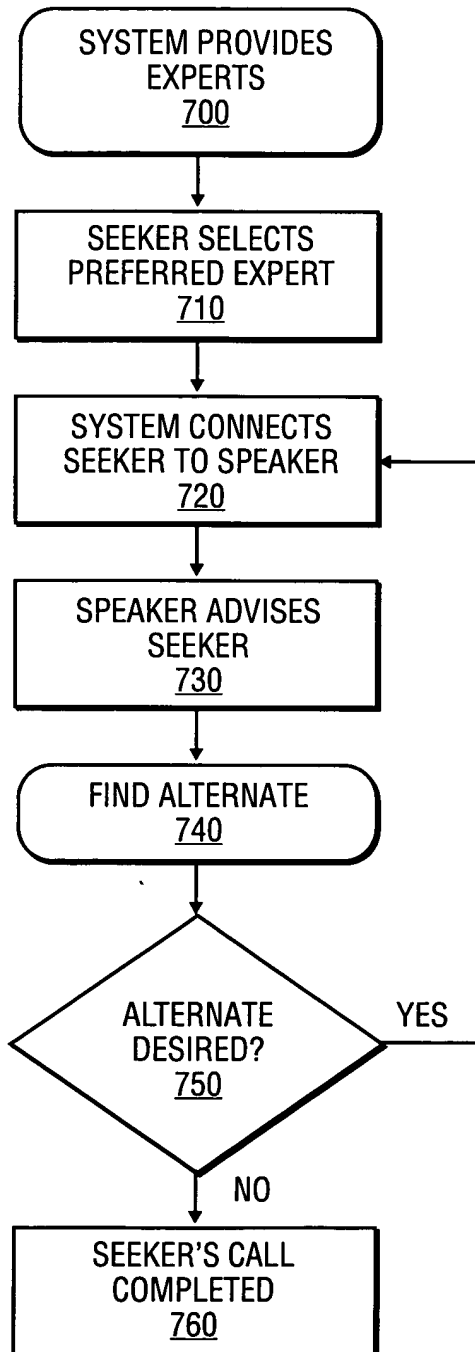


FIG. 7

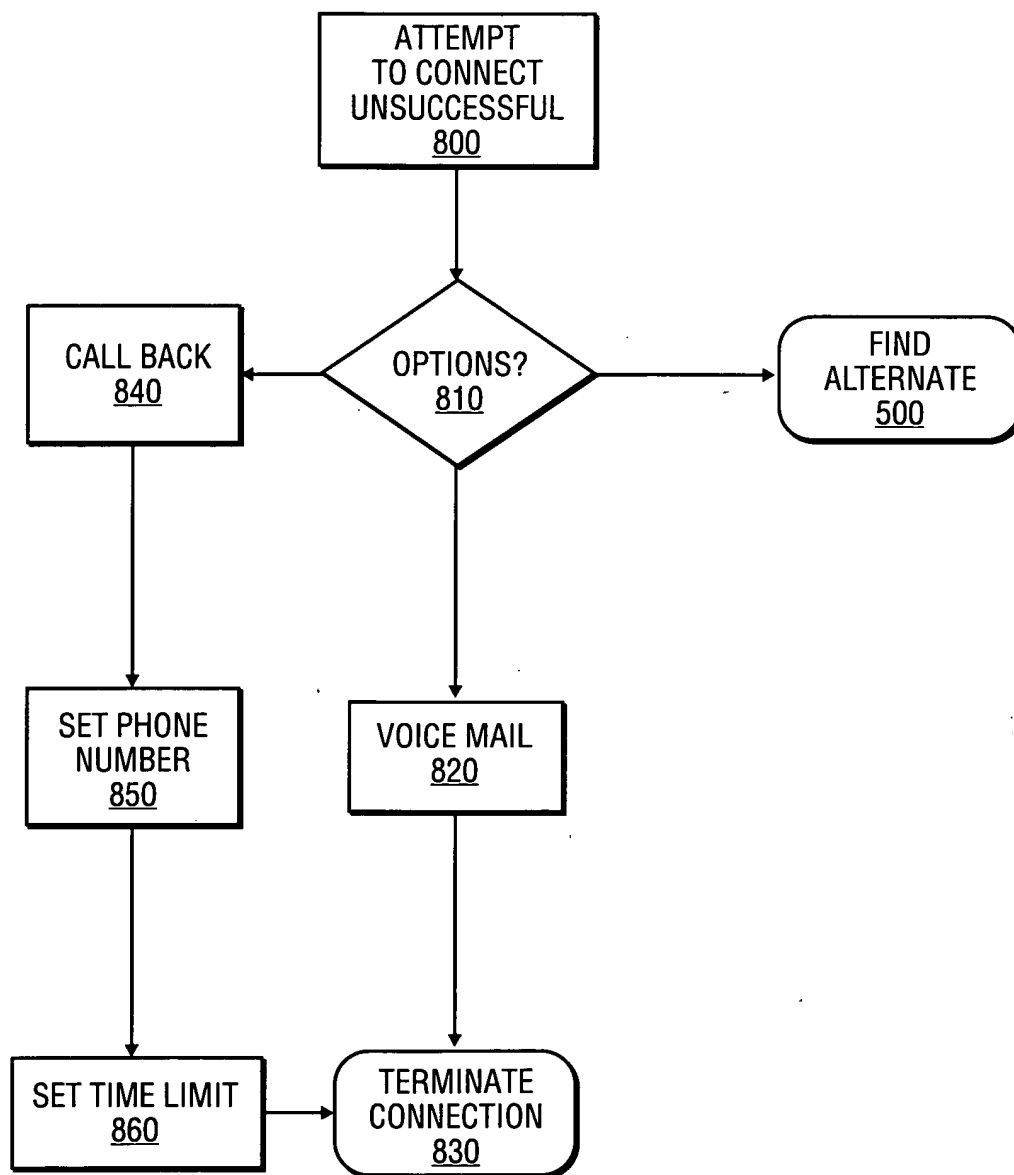


FIG. 8